AMENDMENTS TO THE CLAIMS

This listing of the claims replaces all prior listings and versions:

1. (withdrawn – currently amended): A method for making an array, the method comprising:

(a) isolating a plurality of cellular polynucleotide sequences consisting of sequences corresponding to accessible regions of cellular chromatin and are isolated based on their altered reactivity to a probe of chromatin structure as compared to reactivity of bulk chromatin with the probe, wherein the polynucleotide sequences are at least 25 nucleotides in length; and

(b) attaching each of the isolated sequences to an address on a solid support.

2. (currently amended): An array comprising a plurality of polynucleotide sequences, wherein:

(a) the polynucleotide sequences consist of polynucleotide sequences corresponding to accessible regions of cellular chromatin and are isolated based on their altered reactivity to a probe of chromatin structure as compared to reactivity of bulk chromatin with the probe, wherein the polynucleotide sequences are at least 25 nucleotides in length; and

(b) each polynucleotide sequence is located at a distinct address on a solid support.

3. (previously presented): The array of claim 2, wherein the sequences are isolated from a plurality of different cell types from an organism.

4. (currently amended): The array of claim 2, wherein the sequences are isolated from a single cell or tissue type from an organism.

5. (previously presented): The array of claim 2, wherein the sequences are isolated according to the following procedure:

(a) isolating, from a first cell, a first plurality of cellular polynucleotide sequences, whereby the sequences correspond to accessible region
of cellular chromatin and are isolated based on their altered reactivity to probe of chromatin structure;

(b) isolating, from a second cell, a second plurality of cellular polynucleotide sequences, whereby the sequences correspond to accessible regions of cellular chromatin and are isolated based on their altered reactivity to probe of chromatin structure;

(c) obtaining sequences that are unique to either the first or second plurality of cellular polynucleotide sequences; and

(d) attaching each of the isolated sequences obtained in step (c) to an address on a solid support.

6. (withdrawn): A method of identifying a target sequence bound by a DNA-binding protein, the method comprising the steps of:

(a) contacting at least one DNA-binding protein with an array according to claim 2, under conditions such that the protein binds to sequences comprising a target sequence bound by the protein;

(b) removing unbound proteins; and

(c) identifying the sequences bound by the protein, thereby identifying target sequences for the protein.

7. (withdrawn): A method of identifying a transcription factor, the method comprising the steps of:

(a) preparing a preparation of proteins from a cell;

(b) contacting the isolated proteins with an array according to claim 2, under conditions such that transcription factors in the protein preparation bind to sequences comprising a target sequence bound by a transcription factor;

(c) removing unbound proteins; and

(d) identifying the proteins bound to the array.

8. (withdrawn): A method for obtaining a regulatory profile of sequences corresponding to accessible regions of cellular chromatin in a cell, the method comprising:

(a) isolating a plurality of polynucleotide sequences from the cell, whereby the sequences correspond to accessible regions of cellular chromatin and are isolated based on their altered reactivity to probe of chromatin structure;

(b) optionally amplifying the sequences obtained in step (a);

(c) optionally labeling the sequences of step (a) or (b);

(d) contacting the sequences of step (a), (b) or (c) with an array according to claim 3; and

(e) identifying the sequences bound on the array, thereby identifying sequences corresponding to accessible regions of cellular chromatin in the cell.

9. (withdrawn): A method for identifying functional binding sites for a DNA-binding protein in a cell, the method comprising:

(a) subjecting a cell to conditions under which DNA-binding proteins are crosslinked to their binding sites in cellular chromatin;

(b) shearing the crosslinked cellular chromatin of step (a);

(c) immunoprecipitating the sheared crosslinked chromatin of step (b) with an antibody which recognizes the DNA-binding protein;

(d) reversing the crosslinks in the immunoprecipitate of step (c);

(e) purifying the DNA from the immunoprecipitated material of step (d);

(f) optionally amplifying the DNA obtained in step (e);

(g) optionally labeling the DNA of step (e) or (f);

(h) contacting the DNA from step (e), (f) or (g) with an array according to claim 2; and

(i) identifying the sequences bound on the array, thereby identifying functional binding sites for the DNA-binding protein in the cell.

10. (withdrawn): A method of identifying a sequence in cellular chromatin, wherein the chromatin is covalently modified, the method comprising:

(a) providing a sample of cellular chromatin;

(b) optionally subjecting the chromatin of step (a) to conditions under which DNA-binding proteins are crosslinked to their binding sites in cellular chromatin;

(c) shearing the cellular chromatin of step (a) or (b);

(d) immunoprecipitating the sheared chromatin of step (c) with an antibody which recognizes a covalent chromatin modification;

(e) purifying the DNA from the immunoprecipitated material of step (d);

(f) optionally amplifying the DNA obtained in step (e);

(g) optionally labeling the DNA of step (e) or (f);

(h) contacting the DNA from step (e), (f) or (g) with an array according to claim 2; and

(i) identifying the sequences bound on the array, thereby identifying sequences in cellular chromatin wherein the chromatin is covalently modified.

11. (withdrawn): A method for characterizing the effects of a molecule on a cell, the method comprising:

(a) contacting the cell with the molecule;

(b) isolating a first plurality of polynucleotide sequences from the cell of step (a), whereby the sequences correspond to accessible regions of cellular chromatin and are isolated

based on their altered reactivity to probe of chromatin;

(c) optionally amplifying the sequences obtained in step (b);

(d) optionally labeling the sequences of step (b) or (c);

(e) contacting the sequences of step (b), (c) or (d) with an array according to claim 2; and

(f) identifying the sequences bound on the array, thereby identifying sequences that are accessible in the cell.

12. (withdrawn): The method of claim 11, further comprising the steps of:

(g) providing cells that have not been contacted with the molecule;

(h) isolating a second plurality of polynucleotide sequences from the cell of step (g), whereby the sequences correspond to accessible regions of cellular chromatin and are isolated based on their altered reactivity to probe of chromatin structure;

(i) optionally amplifying the sequences obtained in step (h);

(j) obtaining sequences that are unique to either the first or second plurality of polynucleotide sequences;

(k) optionally amplifying the sequences obtained in step (j);

(l) optionally labeling the sequences of step (j) or (k);

(m) contacting the sequences of step (j), (k) or (l) with an array according to claim 2; and

(n) identifying the sequences bound on the array, thereby identifying differences in accessible sequences between cells that have and have not been contacted with the molecule.

13. (withdrawn): A method of identifying single nucleotide polymorphisms (SNPs) in regulatory sequences of an individual, the method comprising the steps of:

(a) preparing a library of regulatory DNA sequences from chromatin isolated from cells from the individual;

(b) optionally labeling the sequences of step (a);

(c) hybridizing the sequences of step (a) or (b) to an array according to claim 2 under stringent hybridization conditions, wherein the regulatory DNA sequences of the library hybridize to complementary accessible sequences on the array;

(d) removing regulatory DNA sequences of the library that are not bound to sequences on the array; and

(e) identifying sequences on the array that are not hybridized to regulatory DNA sequences of the library, wherein the unbound sequences on the array suggest the presence of a SNP in regulatory sequences of the individual corresponding to the unbound sequence.

14. (withdrawn): A method for characterizing the effects of a stimulus on a cell, the method comprising:

(a) subjecting the cell to the stimulus;

(b) isolating a first plurality of polynucleotide sequences from the cell of step (a), whereby the sequences correspond to accessible regions of cellular chromatin and are isolated based on their altered reactivity to probe of chromatin structure;

(c) optionally amplifying the sequences obtained in step (b);

(d) optionally labeling the sequences of step (b) or (c);

(e) contacting the sequences of step (b), (c) or (d) with an array according to claim 2; and

(f) identifying the sequences bound on the array, thereby identifying sequences that are effected by the stimulus.

15. (withdrawn): The method of claim 14, further comprising the steps of:

(g) providing cells that have not been subjected to the stimulus;

(h) isolating a second plurality of polynucleotide sequences from the cell of step (g), whereby the sequences correspond to accessible regions of cellular chromatin and are isolated based on their altered reactivity to probe of chromatin structure;

(i) optionally amplifying the sequences obtained in step (h);

(j) obtaining sequences that are unique to either the first or second plurality of polynucleotide sequences;

(k) optionally amplifying the sequences obtained in step (j);

(l) optionally labeling the sequences of step (j) or (k);

(m) contacting the sequences of step (j), (k) or (l) with an array according to claim 2; and

(n) identifying the sequences bound on the array, thereby identifying differences in sequences between cells that have and have not been subjected to the stimulus.